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FastDB - Fast Pairwise Comparison of Sequences

Release 5.4

Results file Seq172-Seq525.res made by tport on Wed 12 May 104 13:44:12-PDT.

Query sequence being compared: US-09-895-814-172 (1-159)

Number of sequences searched: 241

Number of scores above cutoff: 241

Results of the initial comparison of US-09-895-814-172 (1-159) with:

File : US09895814.DEP

Score : 30568

Number of residues searched: 241

Number of sequences above cutoff: 241

Number of scores above cutoff: 241

Similarity matrix : PAM-150

Threshold level of sim.: 16%

Mismatch penalty: 1

Gap penalty: 5.00

Gap size Penalty: 0.05

Cutoff score: 1

Randomization group: 0

SEARCH STATISTICS

Scores: Mean 13 Median 10 Standard Deviation 22.42

Time: CPU Total Elapsed 0:00:00.00

Number of residues: 30568

Number of sequences searched: 241

Number of scores above cutoff: 241

Similarity matrix : PAM-150

Threshold level of sim.: 16%

Mismatch penalty: 1

Gap penalty: 5.00

Gap size Penalty: 0.05

Cutoff score: 1

Randomization group: 0

PARAMETERS

Score: 20

Window size: 159

Joining penalty: 1

K-tuple: 1

Number of sequences found: 1

Number of scores found: 1

Number of matches found: 1

Number of mismatches found: 1

Number of substitutions found: 1

Number of gaps found: 1

Number of frameshifts found: 1

Number of insertions found: 1

Number of deletions found: 1

Number of frameshifts found: 1

Number of insertions found: 1

Number of deletions found: 1

Number of frameshifts found: 1

Number of insertions found: 1

Number of deletions found: 1

Number of frameshifts found: 1

Number of insertions found: 1

Number of deletions found: 1

Number of frameshifts found: 1

Number of insertions found: 1

Number of deletions found: 1

Number of frameshifts found: 1

Number of insertions found: 1

Number of deletions found: 1

Number of frameshifts found: 1

Number of insertions found: 1

Number of deletions found: 1

Number of frameshifts found: 1

Number of insertions found: 1

Number of deletions found: 1

Number of frameshifts found: 1

Number of insertions found: 1

Number of deletions found: 1

Number of frameshifts found: 1

Number of insertions found: 1

Number of deletions found: 1

4 100% similar sequences to the query sequence were found:

Sequence Name	Description	Length	Score	Init.	Opt.	Sig.	Frame
2. US-09-895-814-61 Sequence 617, Application 449	Sequence 617, Application 449	159	159	6.51	0		
3. US-09-895-814-52 Sequence 525, Application 254	Sequence 525, Application 254	159	159	6.51	0		

1. US-09-895-814-172 (1-159)
US-09-895-814-17 Sequence 172, Application US/09895814

Initial Score = 159 Optimized Score = 159 Significance = 6.51
Residue Identity = 100% Matches = 159 Mismatches = 0
Gaps = 0

X NVEASISLVRPHPEYNRFLANDMLIKLDESYESESDTIRSIASQOPTAGNSCLVSGWGLLNGRMPTVLQC
X NVEASISLVRPHPEYNRFLANDMLIKLDESYESESDTIRSIASQOPTAGNSCLVSGWGLLNGRMPTVLQC
X R - * 10 20 30 40 50 60 70

X R 10 20 30 40 50 60 70
X VNVSVSEEVYCSKLVDPYLHPSMFAGGGXQXOSNGDGGPLICNGYLQGLNSFGKAPCGQVGPGVXTN
X VNVSVSEEVYCSKLVDPYLHPSMFAGGGXQXOSNGDGGPLICNGYLQGLNSFGKAPCGQVGPGVXTN
X 80 90 100 110 120 130 140
X LCKPTENIEKTVQAS X
X LCKPTENIEKTVQAS X
X 150 X
X LCKPTENIEKTVQAS X
X 150 X

2. US-09-895-814-172 (1-159)
US-09-895-814-61 Sequence 617, Application US/09895814

Initial Score = 159 Optimized Score = 159 Significance = 6.51
Residue Identity = 98% Matches = 157 Mismatches = 2
Gaps = 0

X AALVMENELFCGVLVHPONVLSAAHCFONSYTIGGLHSLEADQEPGSNVEAISLVRPEYNRFLANDL
X 30 40 50 60 70 80 90
X MIJKLIDESVSDDTISIATASQOPTAGNSCLVSGWGLLNGRMPTVLQCNSVSEEVCSKLVDPYHPS
X 100 110 120 130 140 150 160
X 100 110 120 130 140 150 160
X MFAAGGSOXODSCNGDGGPLICNGYLOGLVSFGKAPCGQVGPGVXTNICKFTWIEKTVQAS
X MRAGGGDQKDSCNGDGGPLICNGYLQGLNSFGKAPCGQVGPGVXTNICKFTWIEKTVQAS1VGGMWC
X 170 180 190 200 210 220 230
X EKHSQPWQVLVASRGRAVCGGYLVHPQWVLAHCRNKSVIL
X 240 250 260 270 280

3. US-09-895-814-172 (1-159)
US-09-895-814-52 Sequence 525, Application US/09895814

Initial Score = 159 Optimized Score = 159 Significance = 6.51
Residue Identity = 98% Matches = 157 Mismatches = 2
Gaps = 0

A 100% identical sequence to the query sequence was found:
4 Sequence Name Description Length Score Init. Opt. Sig. Frame

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

4 Sequence Name Description Length Score Init. Opt. Sig. Frame

X 10
MVEASLSVRHPEYNRPILANDL
AALVMENELFCSGVLVHPQWVLSSAAHCFFQNSYTIGHGLHSLEADQEPGGSQMVBEASLSVRHPEYNRPILANDL
50 60 70 80 90 X 100 110
MLIKLDESVSESDTIRSIASQCPTAGNSCLVSENGLLANGRMPVLCQCVNTSVSEEVCSKLYDPLXHPS
MLIKLDESVSESDTIRSIASQCPTAGNSCLVSENGLLANGRMPVLCQCVNTSVSEEVCSKLYDPLXHPS
120 130 140 150 160 170 180
MLIKLDESVSESDTIRSIASQCPTAGNSCLVSENGLLANGRMPVLCQCVNTSVSEEVCSKLYDPLXHPS
100 110 120 130 140 150 X
MFCAGGGQDXDSCNEDSGP LICNGYLQGLIVSFGAKPCQGVGVYTNLCKRPTEWIKTVQAS
MFCAGGGQDXDSCNEDSGP LICNGYLQGLIVSFGAKPCQGVGVYTNLCKRPTEWIKTVQAS
190 200 210 220 230 240 250 X